

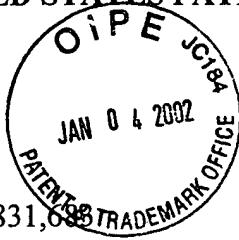
PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

O. FAMODU ET AL.

APPLICATION NO.: 09/831,688



CASE NO.: BB1270

GROUP ART UNIT: UNKNOWN

INTERNATIONAL FILING DATE: 09 NOV 99 EXAMINER: INDIA L. EVANS

FOR: PLANT AMINOACYL-tRNA SYNTHETASES

STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)

Assistant Commissioner for Patents
 Washington, DC 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

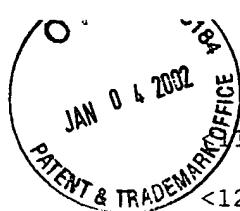
The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,

Thomas M. Rizzo, Ph.D.
 Attorney For Applicants
 Registration No. 41,272
 Telephone: 302-892-7760
 Facsimile: 302-892-1026

Dated: November 15, 2001

SEQUENCE LISTING



10> E. I. du Pont de Nemours and Company
<120> Plant Aminoacyl-tRNA Synthetases

<130> BB1270

<140> US/09/831,683
<141> 2001-05-10

<150> 60/107,789
<151> 1998-11-10

<160> 38

<170> Microsoft Office 97

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<213> Oryza sativa

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<212> PRT

<213> Oryza sativa

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Met Ala Val Gly Gln Ala Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile
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Ile Glu Ser Ile Ser Val Ala Gly Pro Gly Tyr Ile Asn Ile Thr Leu
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Ile Lys Thr Trp Ala Pro Ile Leu Pro Val Lys Arg Ala Val Leu Asp
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Val Glu Val Leu Arg Arg Asn His Val Gly Asp Trp Gly Thr Gln Phe
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Gly Met Leu Ile Glu Phe Leu Phe Glu Gln Phe Pro Asp Trp Glu Asp
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Lys Lys Arg Phe Asp Asp Asp Pro Asp Phe Lys Glu Arg Ala Arg Gln
210 215 220
Ala Val Val Arg Leu Gln Gly Glu Asp Lys Tyr Arg Ala Ala Trp
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Arg Leu Asn Val Lys Leu Glu Glu Lys Gly Glu Ser Phe Tyr Asn Pro
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Tyr Ile Pro Pro Val Leu Glu Glu Leu Thr Asn Lys Gly Leu Ile Val
275 280 285
Glu Ser Lys Gly Ala Arg Val Ile Phe Val Glu Asp His Pro Leu Ile
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Val Ile Lys Gln Asp Gly Gly Phe Asn Tyr Ala Ser Thr Asp Leu Ala
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Ala Leu Trp Tyr Arg Leu Asn Val Glu Lys Ala Glu Trp Ile Ile Tyr
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Val Thr Asp Val Gly Gln Gln Arg His Phe His Met Leu Phe Thr Ala
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Gly Asn Gly Gln Ile Ala Asp Trp Thr Asp Asp Glu Leu Asp Arg Thr
420 425 430

Ser Glu Ala Ile Gly Tyr Gly Ala Val Lys Tyr Ser Asp Leu Lys Asn
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Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile Cys
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Ser Ile Ile Arg Lys Ala Ser Lys Asp Val Glu Lys Leu Lys Met Thr
485 490 495

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Leu Ile Gln Phe Thr Glu Val Val Glu Gln Ala Cys Ala Asp Leu Gln
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Pro His Arg Leu Cys Asp Tyr Leu Tyr Ser Leu Ser Leu Thr Phe Ser
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<213> Glycine max

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35 40 45
Gln His Phe Asp Met Leu Phe Lys Ala Tyr Arg Arg Ala Gly Trp Leu
50 55 60
Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
65 70 75 80
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195 200 205
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210 215 220
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Leu Gly Asp Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
 50 55 60

Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu
 65 70 75 80

Glu Leu Glu Gln Thr Ser Lys Ala Val Gly Tyr Gly Ala Val Lys Tyr
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Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Asp
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Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala
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His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Met Asp Val Glu
 130 135 140

Glu Leu Lys Val Ser Gly Asn Ile Ser Leu Ala His Pro Asp Glu Arg
 145 150 155 160

Val Leu Gly Leu Tyr Leu Ile Arg Tyr Ala Glu Ile Val Glu Glu Ala
165 170 175

Cys Thr Asn Leu Leu Pro Ser Val Leu Cys Glu Tyr Leu Tyr Asn Leu
 180 185 190

Ser Glu Met Phe Thr Arg Phe Tyr Thr Asn Cys Gln Val Val Gly Ser
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Pro Glu Glu Pro Ser Arg Leu Leu Leu Cys Glu Ala Thr Gly Val Val
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<213> Zea mays

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35 40 45

Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser
50 55 60

Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val
65 70 75 80

Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu
85 90 95

Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu
100 105 110

Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu
115 120 125

Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr
130 135 140

Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu
145 150 155 160

Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly
165 170 175

Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp
180 185 190

Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val
195 200 205

Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
210 215 220

Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly
225 230 235 240

Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn
245 250 255

Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys
260 265 270

Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu
275 280 285

Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr
290 295 300

Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg
305 310 315 320

Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met
325 330 335

Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu
340 345 350

Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg
355 360 365

Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr
370 375 380

Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val
385 390 395 400

Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr
405 410 415

Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu
420 425 430

Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu
435 440 445

Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg
450 455 460

Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala
465 470 475 480

Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu
485 490 495

Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro
500 505 510

Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe
515 520 525

Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg
530 535 540

His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn
545 550 555 560

Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ile Asn Lys Gly Glu
565 570 575

Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
580 585 590

Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu
595 600 605

Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
610 615 620

Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
625 630 635 640

Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
645 650 655

Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
660 665 670

Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
675 680 685

Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala
690 695 700

Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
705 710 715

<210> 11

<211> 1920

<212> DNA

<213> Oryza sativa

<220>

<221> unsure

<222> (139)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (238)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (431)

<223> n = A, C, G or T

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cgaaggcccg gatgtcggtg gggatatgg gcccgcgc cagtccgagc gcaattcgat 420
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cattggcaag tgggggactg cttcagatgc agaaatacaa caggagttag agaaggggac 600
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tcgtggtgag gtcagttgga acttagacac gcttggtgat ttctgtgatta tgagaagcaa 720

tggccagcca gtgtataact tctgtgtcac agttgatgat gctaccatgc gcatctctca 780
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<210> 12
<211> 555
<212> PRT
<213> Oryza sativa

<220>
<221> UNSURE
<222> (130)
<223> Xaa = ANY AMINO ACID

<400> 12
Leu Arg Ile Arg Leu Leu Pro Glu Val Pro Pro Arg Leu Leu Arg Pro
1 5 10 15

His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Arg Arg
20 25 30

His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala
35 40 45

Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr
50 55 60

Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp
65 70 75 80

Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser
85 90 95

Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly
100 105 110

Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys
115 120 125

Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe
130 135 140

Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys

145	150	155	160
Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala			
165	170	175	
Glu Ile Gln Gln Glu Leu Glu Lys Gly Thr Pro Tyr Thr Tyr Arg Phe			
180	185	190	
Arg Val Pro Lys Glu Gly Ser Leu Lys Ile Asn Asp Leu Ile Arg Gly			
195	200	205	
Glu Val Ser Trp Asn Leu Asp Thr Leu Gly Asp Phe Val Ile Met Arg			
210	215	220	
Ser Asn Gly Gln Pro Val Tyr Asn Phe Cys Val Thr Val Asp Asp Ala			
225	230	235	240
Thr Met Arg Ile Ser His Val Ile Arg Ala Glu Glu His Leu Pro Asn			
245	250	255	
Thr Leu Arg Gln Ala Leu Ile Tyr Lys Ala Leu Gly Phe Pro Met Pro			
260	265	270	
Ser Phe Ala His Val Ser Leu Ile Leu Ala Pro Asp Arg Ser Lys Leu			
275	280	285	
Ser Lys Arg His Gly Ala Thr Ser Val Gly Gln Tyr Lys Glu Met Gly			
290	295	300	
Tyr Leu Pro Gln Ala Met Val Asn Tyr Leu Ala Leu Leu Gly Trp Gly			
305	310	315	320
Asp Gly Thr Glu Asn Glu Phe Phe Thr Ile Asp Asp Leu Val Glu Lys			
325	330	335	
Phe Thr Ile Asn Arg Val Asn Lys Ser Gly Ala Val Phe Asp Ala Val			
340	345	350	
Lys Leu Lys Trp Met Asn Gly Gln His Leu Arg Ser Phe Pro Pro Asp			
355	360	365	
Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr Gly Ile Leu			
370	375	380	
Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu Leu Leu Lys			
385	390	395	400
Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Leu Ser Asn Leu			
405	410	415	
Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu Ala Lys Ser			
420	425	430	
Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu Ile Ser Ala			
435	440	445	
Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly Arg Asp Gly			
450	455	460	
Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys Arg Lys Gly			

465	470	475	480
Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His			
485	490	495	
Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr			
500	505	510	
Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg			
515	520	525	
Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln			
530	535	540	
Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser			
545	550	555	
<210> 13			
<211> 731			
<212> DNA			
<213> Glycine max			
<400> 13			
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<211> 404			
<212> PRT			
<213> Glycine max			
<400> 14			
Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly			
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Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly			
20	25	30	
Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr			
35	40	45	
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu			
50	55	60	
Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg			
65	70	75	80
Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His			
85	90	95	

Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu
100 105 110

Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr
115 120 125

Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala
130 135 140

Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu
145 150 155 160

Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr
165 170 175

Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn
180 185 190

Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile
195 200 205

Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr
210 215 220

Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile
225 230 235 240

Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser
245 250 255

Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn
260 265 270

Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe
275 280 285

Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys
290 295 300

Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln
305 310 315 320

His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu
325 330 335

Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile
340 345 350

Gln Asp Ala Val Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp
355 360 365

Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr
370 375 380

Leu Ala Ser Ala Glu Gly Lys Pro Ile Leu Glu Asp Gly Val Ser Glu
385 390 395 400

Val Ala Lys Ser

<210> 15
<211> 407
<212> DNA
<213> Triticum aestivum

<220>
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<222> (14)
<223> n = A, C, G or T

<220>
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<223> n = A, C, G or T

<220>
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<222> (399)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (401)
<223> n = A, C, G or T

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gcaaggacgc gattcgcgcc gtcaccaaca gggaatcttc atcttggttc cctacgtacg 180
gccctttca attacctgat tgcaaaagct acacgcggta aattcatcct acgcataagag 240
gacacagatn agtcaaggac tgttcctgggt gcgattgaaa aactctgcgc tgnnttgaga 300
tgggggggtt taaaaaggga taaaagggtc ggtccccaat ngaccgcaan ngggccttc 360
aaaaatctca aaagacttt aangttataa aaaaaaacnc nccataa 407

<210> 16
<211> 79
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (55)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (69)
<223> Xaa = ANY AMINO ACID

<400> 16
Lys Phe Gln Asn Ser Leu Ser Glu Arg Leu Pro Ala Arg Thr Arg Phe
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Ala Pro Ser Pro Thr Gly Asn Leu His Leu Gly Ser Leu Arg Thr Ala
20 25 30

Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu
35 40 45

Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu
50 55 60

Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys
65 70 75

<210> 17
<211> 2387
<212> DNA
<213> Zea m

<400> 17
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gcggggcgctg catgtcttaa tgccatcgaa gctcaacgc cccgtcaaat tggggaaagag 180
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gacaccatt tgacgcaaac tcaatttaggg ggagaatgac attacatcat tataattaa 2220
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tcgaatcccc tgagtcccaa tgcattatgc tggatgttc ggctgcagac atattgtgaa 2340
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<210> 18
<211> 495
<212> PRT
<213> Zea mays

<400> 18

Met Leu Leu Arg Asp His Val Thr Asn Gly Ser Thr Val Ala Ala Met
1 5 10 15

Asn Ser Ala Ser Val Ala Glu Trp Ala Thr Ser Leu Ser Leu Leu Phe
20 25 30

Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
35 40 45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
50 55 60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
65 70 75 80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
85 90 95

Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
100 105 110

Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Glu Leu Cys
115 120 125

Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
130 135 140

Asn Ser Ile Ser Ala Leu Lys Arg Tyr Gln Ile Ala Lys Val Tyr Arg
145 150 155 160

Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
165 170 175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
180 185 190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
195 200 205

Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
210 215 220

Cys Gly Val Pro Pro Gln Lys Phe Arg Thr Val Cys Ser Ser Ile Asp
225 230 235 240

Lys Leu Asp Lys Gln Thr Phe Glu Gln Val Lys Lys Glu Leu Val Asp
245 250 255

Glu Lys Gly Ile Ser Asn Glu Thr Ala Asp Glu Ile Gly Asn Leu Val
260 265 270

Lys Thr Arg Gly Pro Pro Leu Glu Val Leu Met Glu Leu Arg Lys Glu
275 280 285

Gly Ser Lys Phe Met Asn Asn Val Gly Ser Val Ala Ala Leu Asn Glu
290 295 300

Leu Glu Ile Leu Phe Lys Ala Leu Asp Lys Ala Asn Ala Ile Ser Lys
305 310 315 320

Ile Thr Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly
325 330 335

Val Ile Tyr Glu Ala Val Phe Lys Gly Ala Ala Gln Val Gly Ser Ile
340 345 350

Ala Ala Gly Gly Arg Tyr Asp Asn Leu Val Gly Met Phe Ser Gly Lys
355 360 365

Gln Ile Pro Ala Val Gly Val Ser Leu Gly Ile Glu Arg Val Phe Ala
370 375 380

Ile Met Glu Gln Gln Glu Lys Glu Arg Asn Glu Lys Ile Arg Pro Thr
385 390 395 400

Glu Thr Glu Val Leu Val Ser Ile Leu Gly Lys Asp Leu Thr Leu Ala
405 410 415

Ala Glu Leu Val Ser Glu Leu Trp Asn Ala Gly Ile Lys Ala Glu Phe
420 425 430

Lys Leu Thr Thr Arg Val Ala Asn His Ile Lys Tyr Ala Leu Gln Ser
435 440 445

Ser Ile Pro Trp Met Val Leu Val Gly Glu Ser Glu Leu Gln Lys Gly
450 455 460

Thr Val Lys Leu Lys Asp Val Glu Ala Asn Gln Glu Glu Val Asp
465 470 475 480

Arg Lys Asp Phe Val Arg Glu Leu Lys Lys Arg Leu Ser Lys Ser
485 490 495

<210> 19

<211> 754

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (18)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (610)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (713)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (720)

<223> n = A, C, G or T

<220>

<221> unsure

<222> (740)

<223> n = A, C, G or T

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aaaagagaan ggtctgttac cgggaagctt aacttgcaaa tagatgacat tgtgtgtgcc 660
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<211> 243

<212> PRT

<213> Glycine max

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<222> (6)

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<222> (238)

<223> Xaa = ANY AMINO ACID

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20 25 30

Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
35 40 45

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
50 55 60

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
65 70 75 80

Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
85 90 95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser
100 105 110

Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys
115 120 125

Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly
130 135 140

Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly
145 150 155 160

Lys Leu Arg Ala Ile Cys Gly Gly Arg Tyr Asp His Leu Phe Ser
165 170 175

Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp
180 185 190

Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu
195 200 205

Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys
210 215 220

Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile
225 230 235 240

Val Glu Val

<210> 21

<211> 1164

<212> DNA

<213> Triticum aestivum

<400> 21

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tgacaagctg gggaaactga gtaggagaaga aattgagaag gaattgattt caactggct 180

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tgctgagcaa	tatggttatt	ctgattggat	ctgttgcgt	gcatctgtt	ttcgtggcct	360
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ctgtggctt	ggatttggag	atgctgtcat	agtggagctg	ctgaaaagaaa	agggtcttt	540
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gccagcatct	agtgttgc	cctgtctcg	gaagaaggc	agatctgtag	accttggaga	660
agacaagcgt	ctgaaatggg	tgttcaaaca	tgctgagagg	ataaacgcta	gcaggctgat	720
cttgggg	aaatccgagt	gggagcgagg	catggtccgt	gtgaagatac	tatcaaccag	780
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ttcacgtcgt	gtatacaaac	aattaggtgg	cttgaatgc	tattgccatc	ttctttcgga	960
tcattcacct	tgcaacaaac	aaagaaattg	taggtttgc	cattcacca	catgtattga	1020
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<210> 22

<211> 271

<212> PRT

<213> Triticum aestivum

<400> 22

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	20					25						30			

Phe	Thr	Gln	Val	Cys	Val	Ile	Val	Asp	Lys	Leu	Gly	Lys	Leu	Ser	Arg
				35				40				45			

Glu	Glu	Ile	Glu	Lys	Glu	Leu	Ile	Ser	Thr	Gly	Leu	Ser	Ser	Glu	Ala
		50				55					60				

Val	Gln	Gly	Ile	Ile	Glu	Val	Leu	Ser	Leu	Lys	Ser	Leu	Ser	Lys	Leu
	65				70				75			80			

Glu	Glu	Val	Leu	Gly	Ser	Gly	Val	Glu	Ala	Val	Ala	Asp	Leu	Lys	Lys
				85				90				95			

Leu	Phe	Ser	Leu	Ala	Glu	Gln	Tyr	Gly	Tyr	Ser	Asp	Trp	Ile	Cys	Phe
				100				105				110			

Asp	Ala	Ser	Val	Val	Arg	Gly	Leu	Ala	Tyr	Tyr	Thr	Gly	Ile	Val	Phe
				115				120				125			

Glu	Ala	Phe	Asp	Arg	Glu	Gly	Glu	Leu	Arg	Ala	Ile	Cys	Gly	Gly	Gly
				130				135			140				

Arg	Tyr	Asp	Arg	Leu	Leu	Ser	Thr	Phe	Gly	Thr	Glu	Asp	Val	Pro	Ala
	145					150			155			160			

Cys	Gly	Phe	Gly	Phe	Gly	Asp	Ala	Val	Ile	Val	Glu	Leu	Leu	Lys	Glu
				165					170			175			

Lys	Gly	Leu	Leu	Pro	Asp	Leu	Pro	Arg	Gln	Ile	Asp	Asp	Ile	Val	Phe
				180				185			190				

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys
195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu
210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile
225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile
245 250 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln
260 265 270

<210> 23

<211> 913

<212> DNA

<213> Zea mays

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ttaagagtga tggtgccct aactatgcct caacagactt aactgctctt tggtatcgcc 180
tcaatgtga gcaggcagag tggatcatat atgttacaga tggatgtcag cagcagcact 240
ttgacatggc tttcagtgc gcaaagatgg ccgggtggct cccagatcca agtggaaaaga 300
agtttccgaa aacaagccat gttggatttg gtcttgcata tggatcaaga tggcaagcgg 360
ttccgaaccc gcagttactga ggttggcata ttggtagagc tacttgcata ggctaaatct 420
cgaggcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480
gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540
ctaaaaata acaggctcac taattacaca tttagtttg aacaatgtc gagcgataag 600
ggaaatactg ctgtgtaccc tcagttatgc catgctcgta tttgttccat tattcgaaa 660
tccaacaaga acgtggnaga ctgaagagat ggagccattt ctctcgacca tccggattag 720
cgctgttggg gctgtatctt anccgatttg cagagttgtt gaagaggatc acgaactact 780
ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840
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ctcgatacn cat 913

<210> 24
<211> 221
<212> PRT
<213> Zea mays

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<223> Xaa = ANY AMINO ACID

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1 5 10 15

Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly
20 25 30

His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
35 40 45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln
50 55 60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe
65 70 75 80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa

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Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu
 100 105 110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
 115 120 125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
 130 135 140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln
 145 150 155 160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys
 165 170 175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser
 180 185 190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile
 195 200 205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp
 210 215 220

<210> 25

<211> 551

<212> DNA

<213> Oryza sp.

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 gtttttgggg attaccagtgt caacaatgct atgagtgtat tttcaagaat aagaggatcc 180
 gcaacaaact tccgtAACcc catggcagtt gggcaggcaa ttgcaaataa cctccccccag 240
 tcaaataatta tcgaatccat ctctgttgcc ggaaatgggtt acattaaacat aacgttatcc 300
 agcaatttggaa ttgcacagag gatacaaaga catgcttgggt tggggaaatc aaaacatggg 360
 gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420
 aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natanccaa 480
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 ngggnacac a 551

<210> 26
 <211> 68
 <212> PRT
 <213> Oryza sp.

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 <222> (51)
 <223> Xaa = ANY AMINO ACID

<400> 26
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Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala
 20 25 30

Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val
 35 40 45

Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala
 50 55 60

Gln Arg Ile Gln
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<210> 27
 <211> 411
 <212> DNA
 <213> Glycine max

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tatgttacag atattgggcga gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180
gcaggttggt taccaaagga tgagaatgcg tatccaaaat gtactcatat aggtttgg 240
cttggttttt gggaaatggg aaaacgattt cggactcgca ncagtnangt tgttcgat 300
gttgattact tgatgaagct aaaangcgct gtaaaattgc cntcttgaaa cgtgatacaa 360
ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g 411

<210> 28
<211> 115

<212> PRT
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<222> (6)
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Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn
20 25 30

Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln
35 40 45

Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu
50 55 60

Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
65 70 75 80

Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa

Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys
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Leu Pro Ser
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<210> 29
<211> 565
<212> DNA
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<222> (555)
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ctcgtagtagc tgaggttggaa gacctacttg atgaggctaa atctcgaagt 180
aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat 240
gaaggaacta agagcaaact tcaaaaggca gtaagatatg ggcgtgtcaa agtatgcggg 300
tctgaaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca 360
agggaaaatac tgctgtcnac ttcaataagc caagcccgta cctcccanca ttcnaaaacc 420
caacatggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480
gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng 540
aaactatnac taccnaagta aaagt 565

<210> 30
<211> 33
<212> PRT
<213> *Triticum* sp.

<400> 30
Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu
1 5 10 15

Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
20 25 30

Leu

<210> 31

<211> 546

<212> DNA

<213> Oryza sp.

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<222> (512)

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tgctacatta agcgtgtatg aagctaaatc tgtggtgcgaa gacaagcttt ctgaggttgc 240
atcaggactc atttctgcctt atgatagcgg tgaacttgcgtt caagcactag ctgagggccg 300
tgatgggtgg cagaagtggg tggaaattt tggcaaatca cttaaaagaa agggaaagtc 360
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caccgtatgc ctcatacaca aagccgnac tgtggagcgg tcactcaaca atccgggttc 480
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aagatc 546

<210> 32

<211> 147

<212> PRT

<213> Oryza sp.

<400> 32

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Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu
20 25 30

Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu
35 40 45

Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu
50 55 60

Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu
65 70 75 80

Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly
85 90 95

Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys
100 105 110

Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly
115 120 125

Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys
130 135 140

Ala Gly Thr
145

<210> 33
<211> 524
<212> DNA
<213> Glycine max

<220>
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<222> (386)
<223> n = A, C, G or T

<220>
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<222> (423)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (459)
<223> n = A, C, G or T

<220>
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<222> (481)
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<400> 33
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tctccgaaca accaccaccc gttcgcgttc gtttcgcgtcc ttctccacc gggaaacctcc 180
acgtcggcgg tgccccaaacg gcccctttca actacttggt cgcaagggtcc aaaggtggga 240
aatttgtgct gagaatttag gacactgact tggagaggtc caagtagggaa gtctgaggag 300
gccatgctca aagatcttcc ttggcttggc cttgattttggg atgaaggggcc tgggtgttgg 360
aggggattat ggtccttaaa aggccatctg agaaggaatt ccttatacaa acaatatgcc 420
ggngaaacta cacaaatccg ggcaagttt accgctgcnt tctgggtccaa agagggaaact 480
nanagnaaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34

<211> 94
<212> PRT
<213> Glycine max

<220>
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<222> (63)
<223> Xaa = ANY AMINO ACID

<400> 34

Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro
1 5 10 15

Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
20 25 30

Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
35 40 45

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser
50 55 60

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
65 70 75 80

Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro
85 90

<210> 35
<211> 506
<212> DNA
<213> Glycine max

<220>
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<223> n = A, C, G or T

<220>
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<222> (483)
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<220>
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<223> n = A, C, G or T

<400> 35

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gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaaat ttatggca 180
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
tgaaagctgt tggtctatct caagaggctg tccaggagct attgcaagtc cttctgtga 300
agtcattgac cgagttagaa gagagacttg ggagagtgaa gaagcagttg ctgatctgaa 360

acagtattct cccttgctga aaaaattgggt tactctaaat ggttcaattt gatgatagtt 420
gttcgaggc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480
gcntctgtgt gtgtcaatac attgn 506

<210> 36
<211> 48
<212> PRT
<213> Glycine max

<400> 36
Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
1 5 10 15

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
20 25 30

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
35 40 45

<210> 37
<211> 577
<212> DNA
<213> Triticum sp.

<220>
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<220>
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<220>
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<220>
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<222> (413)
<223> n = A, C, G or T

<220>
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<222> (469)
<223> n = A, C, G or T

<220>
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<222> (481)
<223> n = A, C, G or T

<220>
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<223> n = A, C, G or T

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<221> unsure
<222> (575)
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<220>
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<223> n = A, C, G or T

<220>
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<222> (551)
<223> n = A, C, G or T

<220>
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<222> (556)
<223> n = A, C, G or T

<220>
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<222> (564)
<223> n = A, C, G or T

<400> 37

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aagctgggaa aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180
tctgaagcag tacagggcat cattgaagtg ctctctctca agtcaactgtc caaacttgaa 240
gaggtgctag gctcagggtg tgaagccgtt gctgacttga agaaccttctt ctgcgttgct 300
gagcaatatg gttattctga ttggatctgt ttgcgtatgcat ctgttggtcg tggccttgca 360
tactacacan gggattgtt ttgaggctt tggataggaa gggaaactga nancatttg 420
gggggggggg aggtatgaca ggctacgtca acatttgaa ctgaagatnt ccaccctgtg 480
nctttggatt tggaaatcctg tcanagtggc ctccnaaaga aaggctttn ctacctgcac 540
tcaaataata nattgntcca ttgncaagac ttgggggg 577

<210> 38
<211> 46
<212> PRT
<213> Triticum sp.

<220>
<221> UNSURE
<222> (38)
<223> Xaa = ANY AMINO ACID

<400> 38

Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr
1 5 10 15

Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys
20 25 30

Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile
35 40 45